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#8

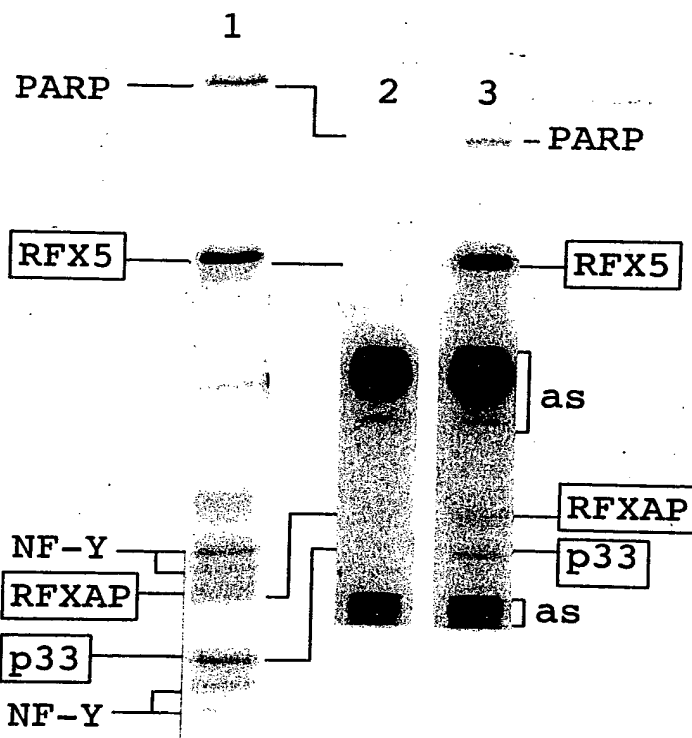


FIG. 1

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FIG. 2A

1
 1
 58
 118
 178
 238
 298
 358
 418
 478
 538
 598
 61

ACGCAGGAAGGAGGCACACCGGGGGTGGCGCAGTGAGAGGGGGCGGACGGCCA
 GGAGGCTGGTGGAGCGACACCCAGGCAGGAGGGGAAGAACTCTCTCCCTTCTGAAC
 CCCCTTTCCCTTGAGAGACGAGTTGGGGGAGTCCTCCACGCATTACCCACTCGGGCCGCA
 AAACTCCCTTCTTTAGCCCTCTGCCCCCGCCCTTGCTTATAAGCCTTTGAGACCGCAGA
 AGGGACCTTGTTGTGGAACGGACGGCCAAAGAGGAAGCCAGATCGCTGAGGGTCCGGTCT
 CCAGTTGCCTCCTGCTATATCCATTGGAAGAGAAAGTTGTGACTTGGGCCCCCAAGT
 TTTGAGAGAACTGGGCTTTCGGCGGGGGACAGAGGAGGCTCGTGGGGAGCTTTCCCC
 ATGGAGCTTACCCAGCCTGCAGAGACCTCATCCAGACCCAGACACCCCTGCCTCAGAA
 M E L T Q P A E D L I Q T Q Q T P A S E
 CTTGGGACCCCTGAAGACCCCGAGAGAGGCTGCAGATGGCTCAGACACTGTGGTCCCTC
 L G D P E D P G E A A D G S D T V V L
 AGTCTCTTTCCCTGCACCCCTGAGCCTGTGAATCCTGAACCGGATGCCAGTGTTCCTCT
 S L F P C T P E P V N P E P D A S V S S
 CCACAGGcagGAGCTCCCTGAAGCACTCCACCACTCTCACCAACCGGACGAGGGAAC
 P Q (A) G S S L K H S T T L T N R Q R G N

1
 2
 3
 4

FIG. 2A

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FIG. 2B

658	GAGGTGTCAGCTCTGCCGGCCACCTAGACTCCCTGTCCATCCACCAGCTCGCAGCACAG	→ 5
81	E V S A L P A T L D S L S I H Q L A A Q	
718	GGGAGCTGGACCAGCTGAAGGAGCATTTGCGGAAAGGTGACAACCTCGTCAACAAGCCA	→ 6
101	G E L D Q L K E H L R K G D N L V N K P	
778	GACGAGCGGGCTTCACCCCCCTCATCTGGGCCTCCGCCTTTGGAGAGATTGAGACCGTT	
121	D E R G F T P L I W A S A F G E I E T V	→ 7
838	CGCTTCCTGCTGGAGTGGGTGCCGACCCCATCTCTGGCAAAGAGCGAGAGCGCC	
141	R F L L E W G A D P H I L A K E R E S A	
898	CTGTCGCTGCCAGCACAGGGGGTACACAGACATTGTGGGGTGTCTGGAGCGTGAC	
161	L S L A S T G G Y T D I V G L L L E R D	→ 8
958	GTGGACATCAACATCTATGATTGGAATGGAGGACGCCACTGCTGTACGCTGTGCGCGGG	
181	V D I N I Y D W N G G T P L L Y A V R G	→ 9
1018	AACCACGTGAAATGCGTTGAGGCCTTGCTGGCCCCGAGGCGGTGACCTCACCACCGAAGCC	
201	N H V K C V E A L L A R G A D L T T E A	
1078	GACTCTGGCTACACCCCGATGGACCTTGCCGTGGCCCTGGGATACCGGAAAGTGCAACAG	→ 10
221	D S G Y T P M D L A V A L G Y R K V Q Q	

FIG. 2B

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FIG. 2C

1138	GTGATCGAGAACCATCCTCAAGCTCTTCCAGAGCAACCTGGTGCCCGCTGACCCCTGAG	
241	<u>V I E N H I L K L F Q S N L V P A D P E</u>	
1198	TGAAGGCCGCCCTGCCGGGACTCAGACACTCAGGGAACAAATGGTCAGCCAGAGCTGGG	*
260		
1258	GAAACCCAGAACTGACTTCAAGGCAGCTTCTGGACAGGTGGTGGAGGGACCCCTTCCC	
1318	AAGAGGAACCAATAAACCTTCTGTGCAG - polyA	

FIG. 2C

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HsREFXANK	MELTQPAEDLIQQTTPASELGDPEDPGEAAAGSDTVLSLFPCTPEPVNPEPDASVSS	60
MmREFXANK	--P--V--N--VPN--P--VPD-E--TRD-SPEN-----DA---A---A---	60
Hs homol	NAFNVFTEVFHIAECNIHTSPSPGIGQVRHVXTP-T	35
Mm homol	ASVLFKAEACNIHTSPSPGIGQVRHVYTP-T	29
HsREFXANK	HHHHT HHHHHHHHHHT	
MmREFXANK	PQaGSSLKHSTLTNRQRGNEVSALPATLDSLSIHQLAQAGELDQLKEHLRKG.....	113
Hs homol	L--F-----S---D-----acpactc	119
Mm homol	TKHF-PI-Q-----KH-----TT-LLAN--V-----MLY-ATRIEQ.....	87
GABPβ	TKHF-PI-Q-----KH-----TT-LLAN--A-----MLY-ATRIEQ.....	81
	EA-RA-QD-EVRILMAN-.....	25
HsREFXANK	ank 1	
MmREFXANK	TT HHHHHHHHT HHHHHHHHTTT TT TT HHHHHHHHT H	170
Hs homol	...DNLVNKPDERGFTPLIWASAFGEIETVRFLLEWGADPHILAKERESALSTGGYT	179
Mm homol	lsgN--I-----M--A-H-Q-AV-E---QN---QL-G-G-----M-----	144
GABPβ	...E-VI-HT--E-----M--A-H-Q-AV-E---QN---QL-G-G-----CSK---	138
	...E-VI-HT--E-----M--A-H-Q-AV-E---QN---QL-G-G-----CSK---	80
	...APETT...-WL-TS--HL-AQY-HFS-TEV--RA-VSRDART-VDRTP-HM-ASE-HA	

FIG. 3A

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	ank 2	ank 3	
	HHHHHHHTT	TT	TTTT HHHHHHHHTT TT TTT HHHHH
HsREFXANK	DIVGLLLERDV	INIYD	WNGTPLL
MmREFXANK	YAVRGNHVC	VEALL	ARGADLTTEADSGYTPMDLA
Hs homol	---	R---	D---
Mm homol	---	XM---	DCG--V-X---
GABPβ	---	KM---	DCG--V-E---
	N---	EV---	KHGA-V-AK-MLKM-A-HW-TEH--QEV--L-IKY--VH-QSKFCK-AF-IS
	HHTT HHHHHHH		
HsREFXANK	VALGYRKVQ	QVIENHILKLFQSNLVPADPE	260
MmREFXANK	---	-----M-S-----R-----T-G-V---	269
Hs homol	---	IEVFNRLSHIC	220
Mm homol	---	GCSDYMLVTDVFERI	218
GABPβ	IDN-NEDLAEILQ		153

FIG. 3B

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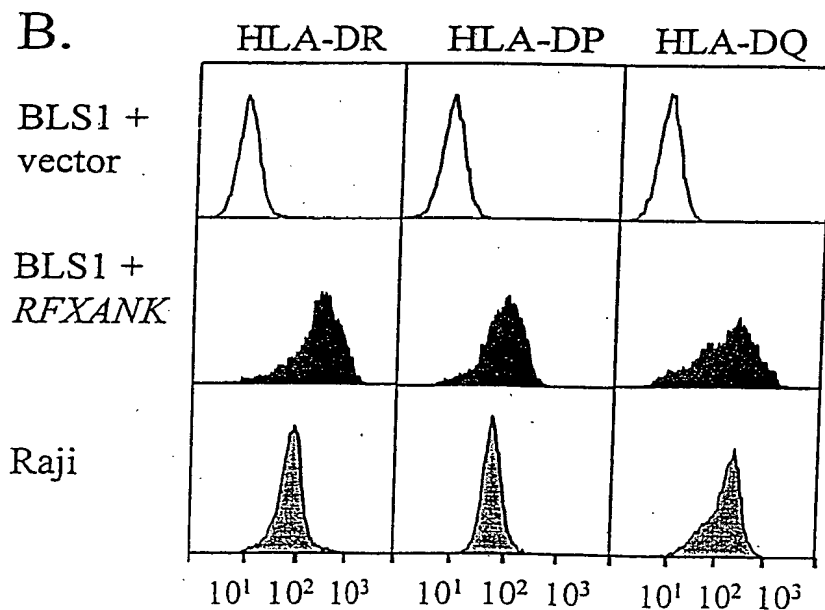
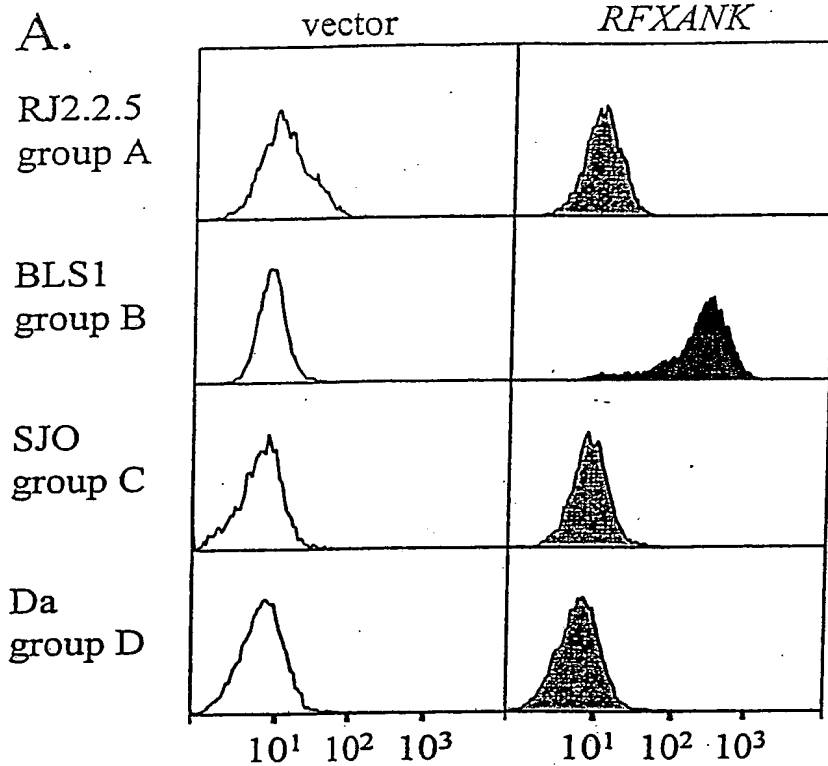


FIG. 4

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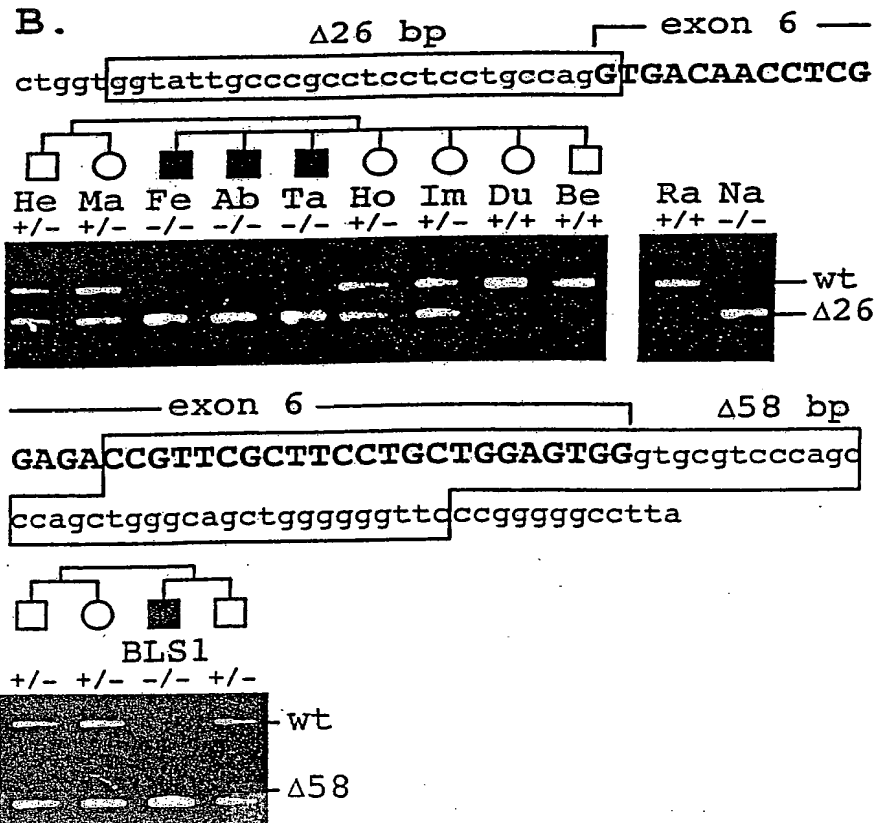
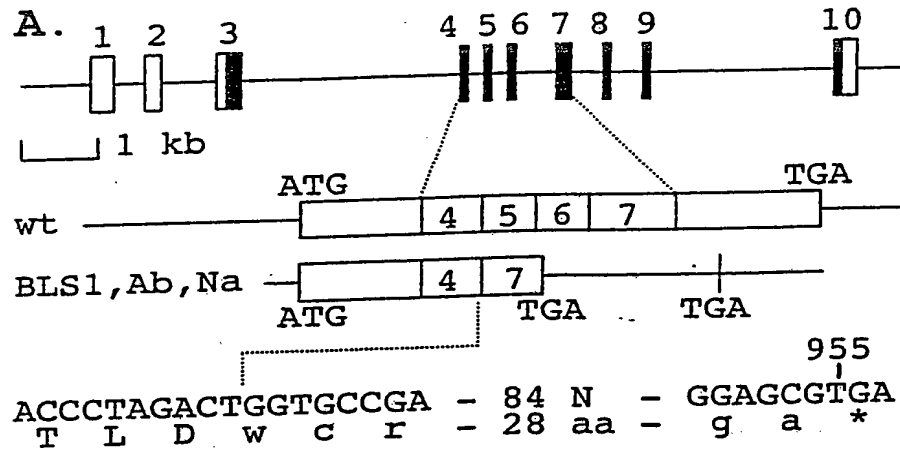
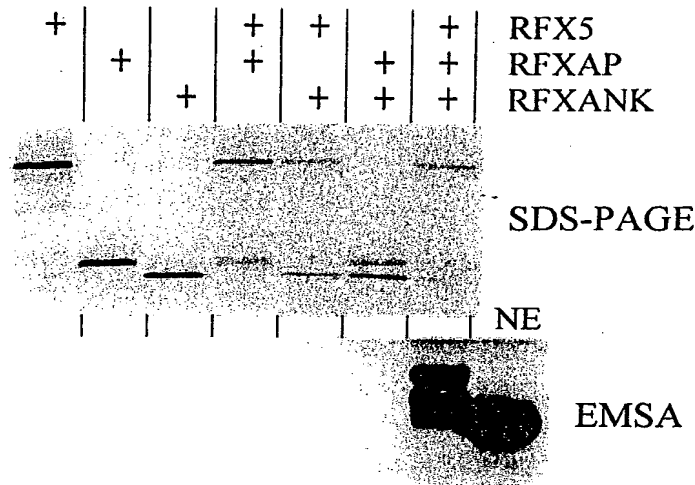


FIG. 5

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A.



B.

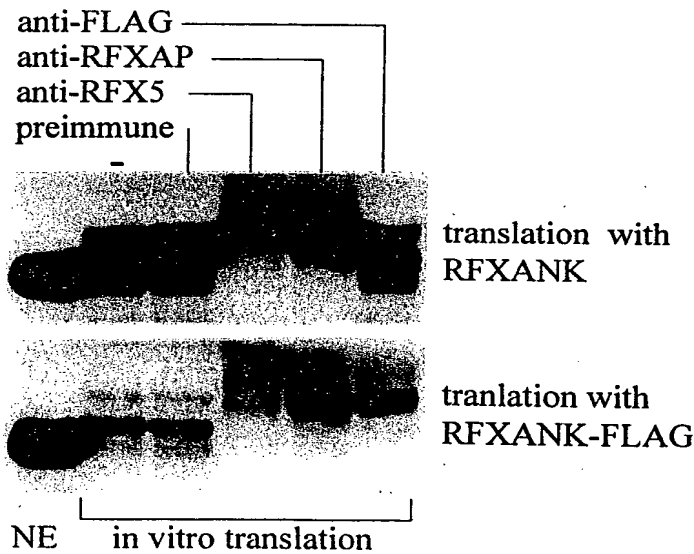


FIG. 6

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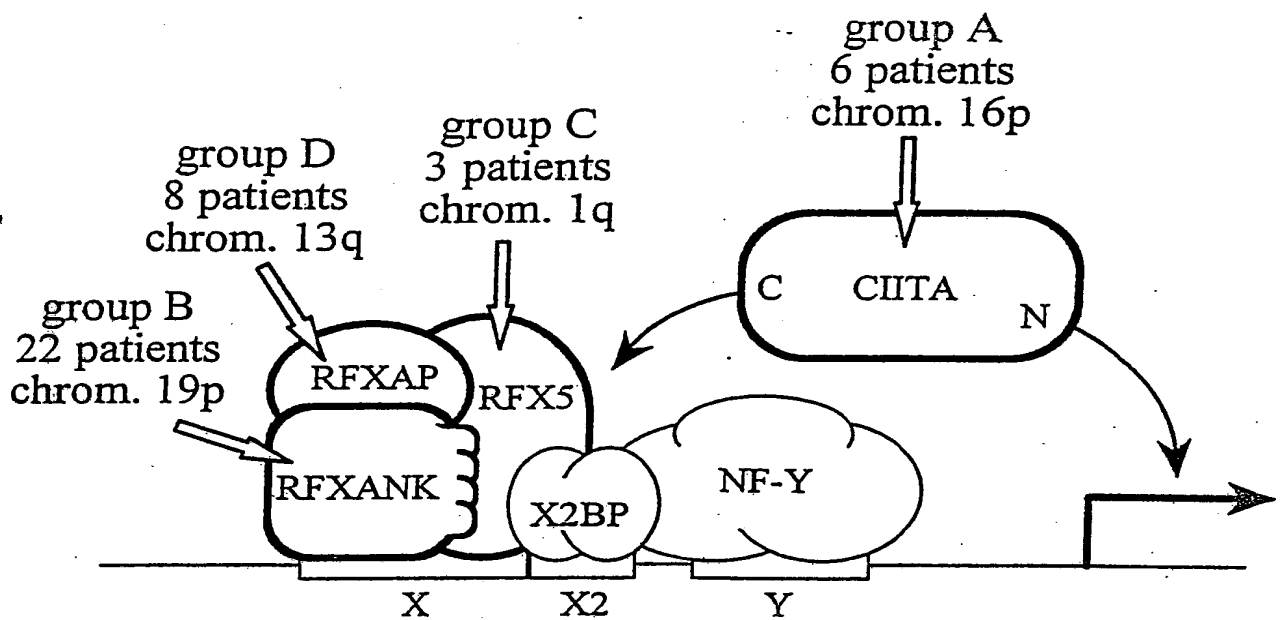


FIG. 7

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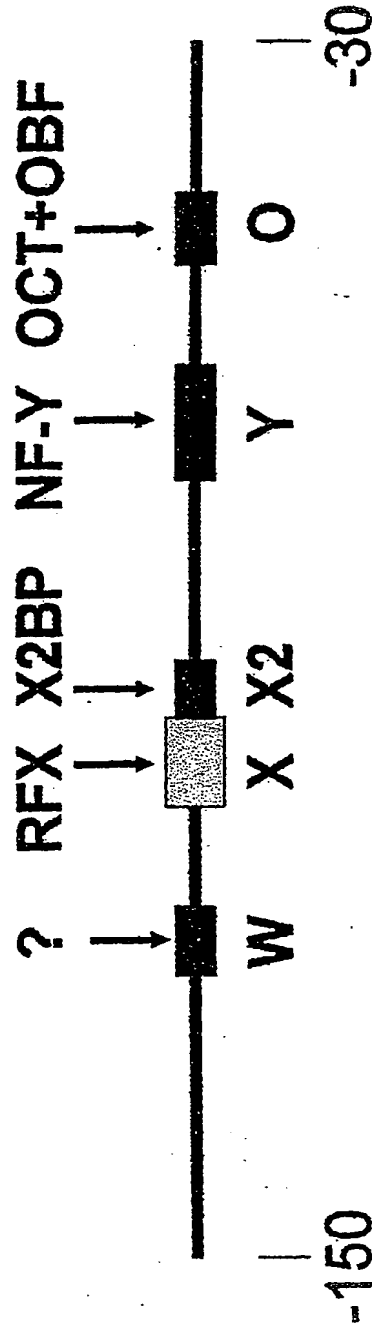


FIG. 8

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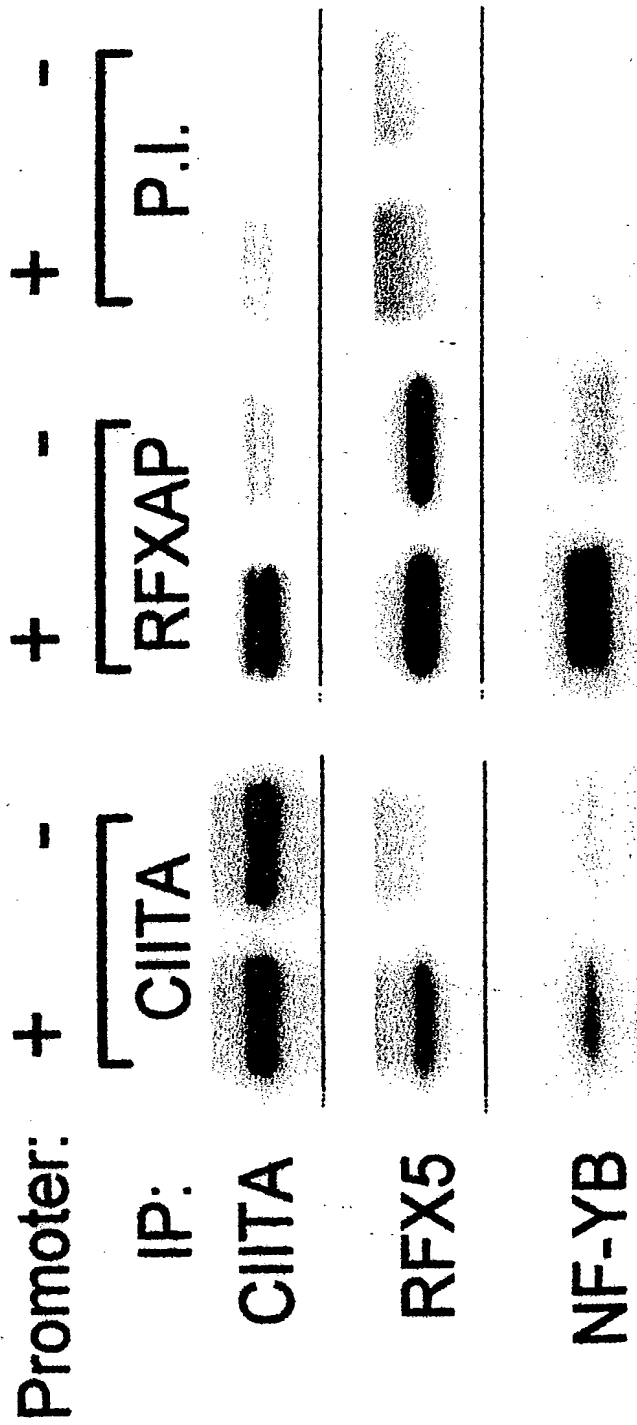


FIG. 9

FIG. 9

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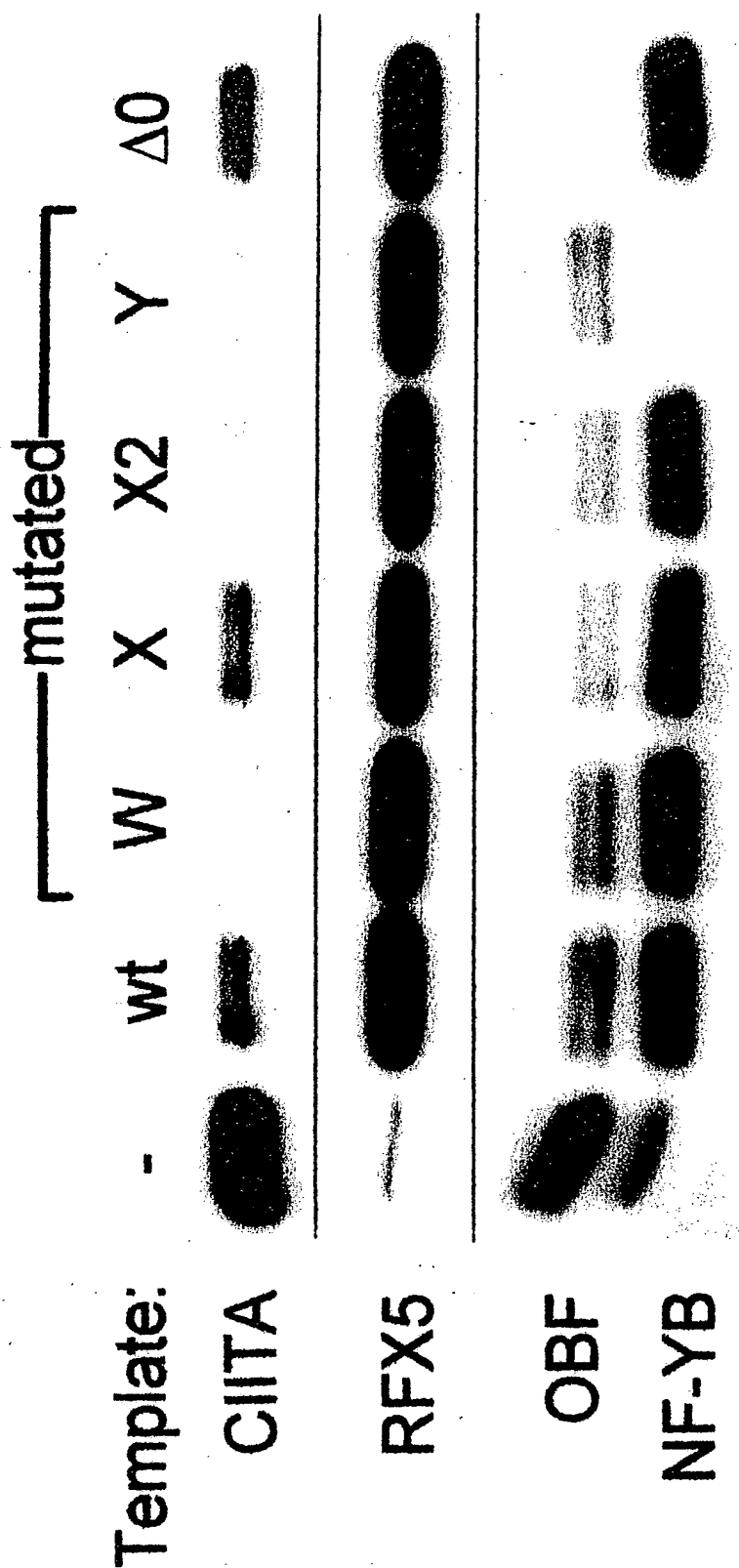


FIG. 10A

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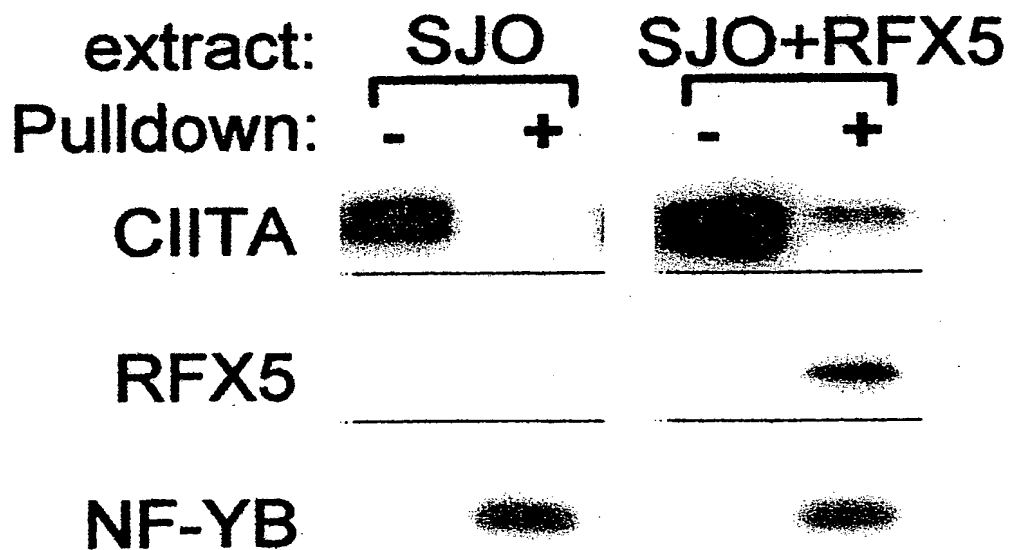


FIG. 10B

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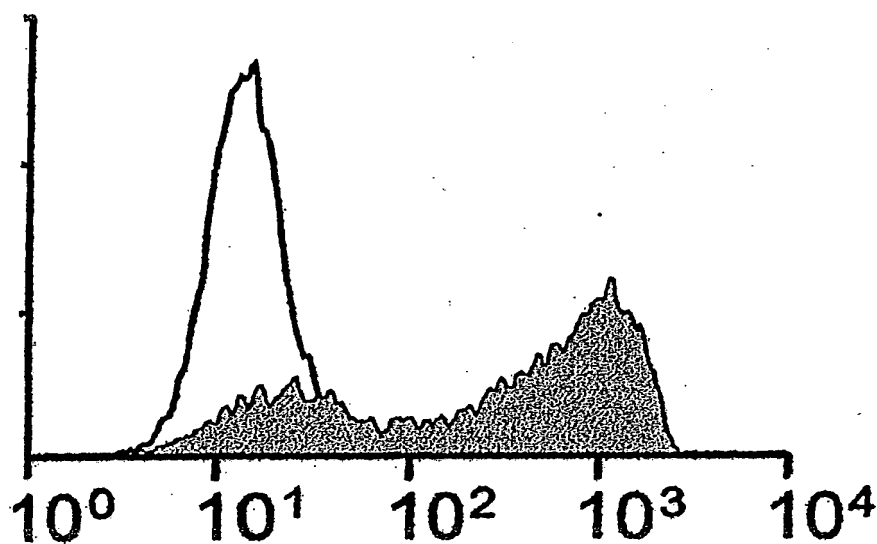


FIG. 10C

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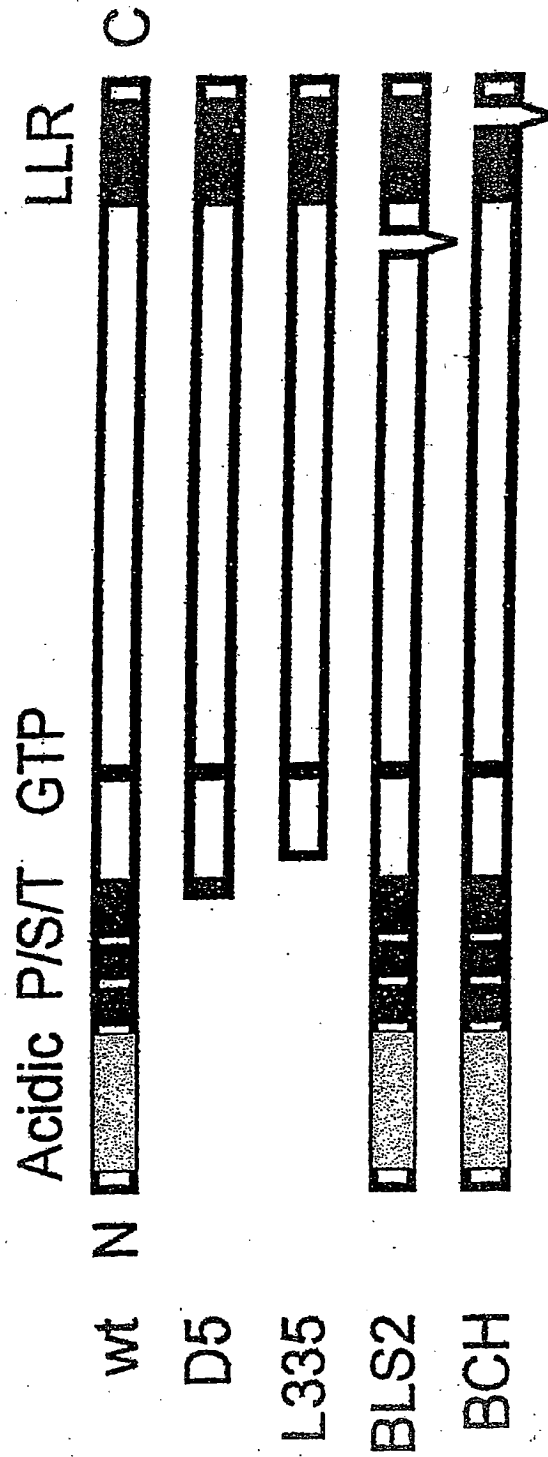


FIG. 11A

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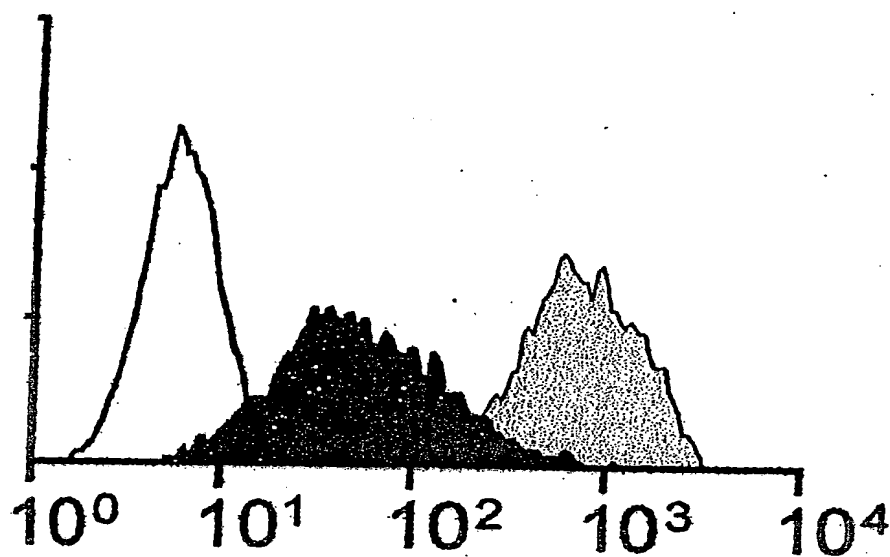


FIG. 11B

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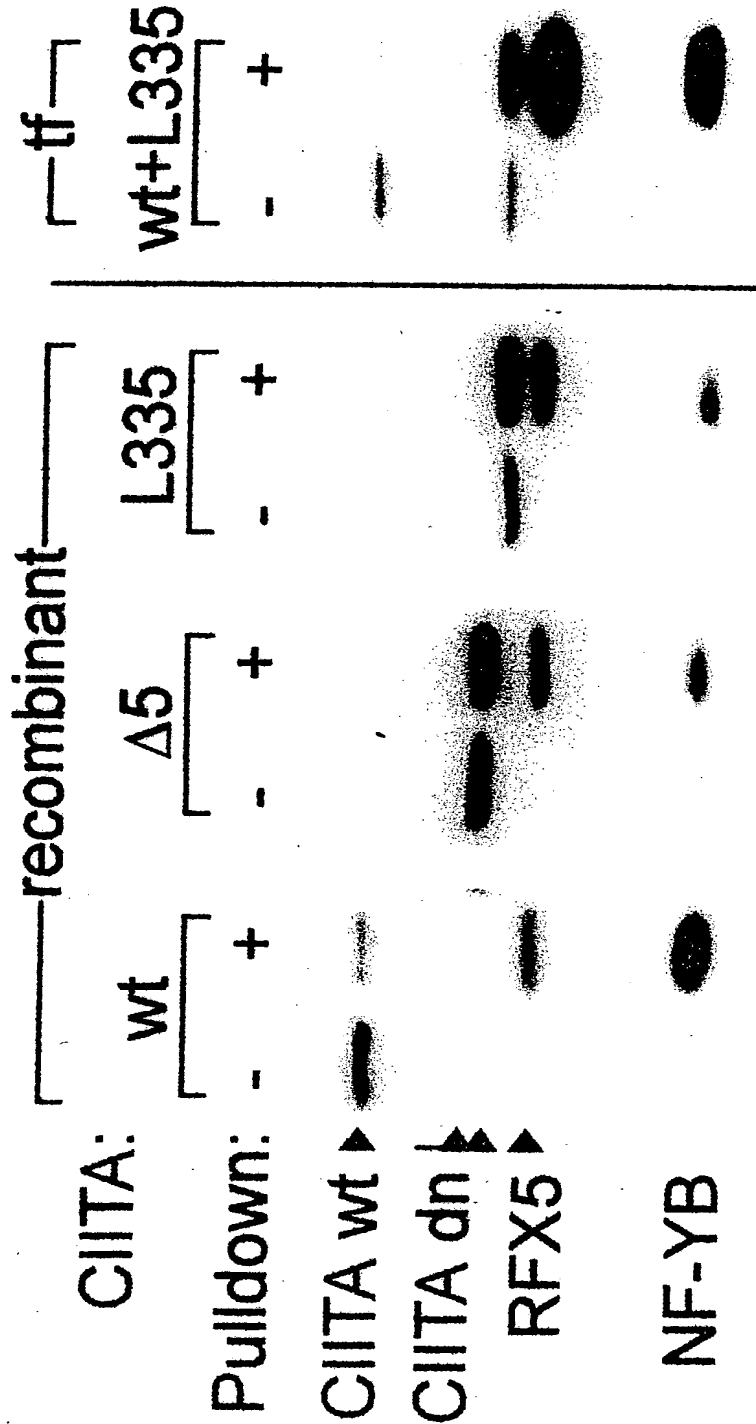


FIG. 11C

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FIG. 11D

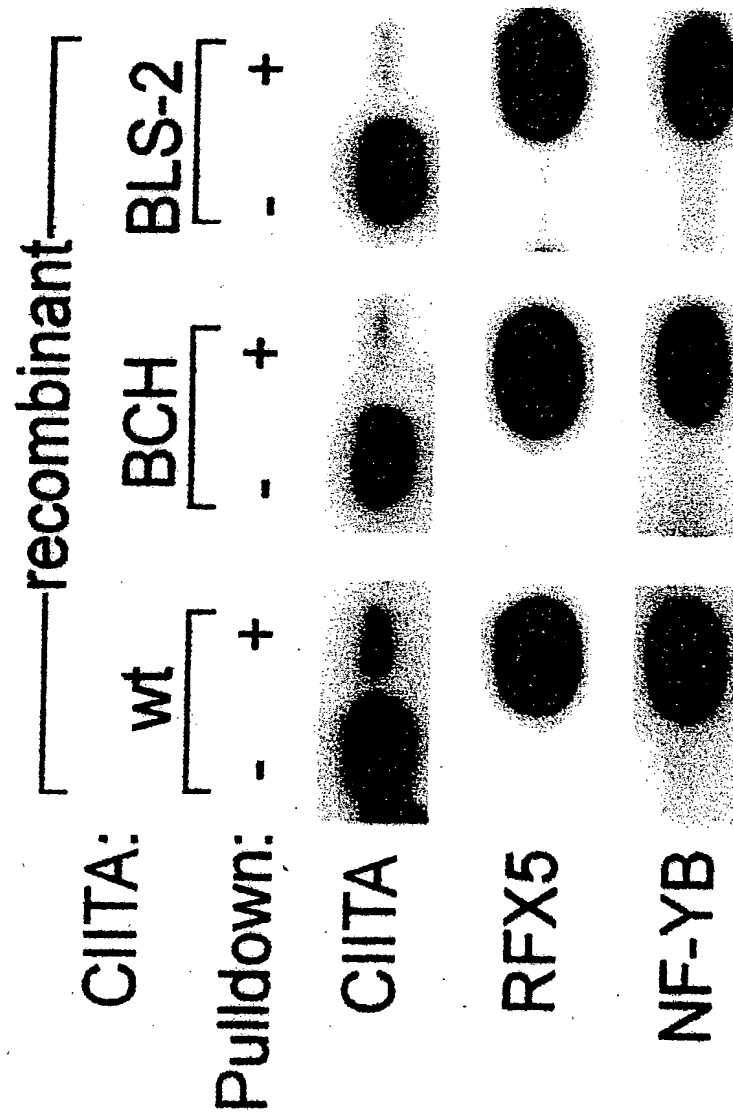


FIG. 11D